Amendments to the Specification:

Please replace on page 1, lines 5-8 with the following amended paragraph:

This application is a continuation of co-pending United States Serial No. 09/747,460, filed January 23, 2001, which is continuation-in-part of United States Serial No. ~~09/490,701~~ 09/490,702, now U.S. Patent No. 6,560,542, filed January 24, 2000, which is incorporated herein in its entirety.

Please replace on page 70, lines 2-14 with the following amended paragraph:

If we chose to apply the template-generating algorithm directly to this series, the search algorithm would begin by looking for two copies of the first half of the series, AIRKSMLRYGHAMQL (SEQ ID NO:95). Next it would assess the starting positions and frequency of occurrence of the substring from which the last amino acid, L has been dropped, i.e., AIRCKSMLRYGHAMQ (SEQ ID NO:96), and so on, looking at each possible substring in the first half of the sequence. The algorithm finds one redundant substring, HAMQ, (SEQ ID NO:98) occurring twice starting at positions 12 and 24. A generalization of this method also allows for the search of substrings that are both "backward" and "forward" in orientation in the original sequence. Such a search of our example string also turns up the twice repeated substring MLRY (SEQ ID NO:99), appearing at starting position 7 in a "forward" orientation and at starting position 29 in a "backward' orientation. Our R_{temp} might then equal one or both of these specific amino acid substrings in some order and orientation.

Please replace on page 70, lines 15-23 to page 71, lines 1-2 with the following amended paragraph:

Transforming the amino acid sequence into a symbolic vector in which each point represents the hydrophobic free energy group membership of the corresponding amino acid sequence, we get: 3132242231433242331222233242l322. A search of this string for redundant substrings yields: 33242 (which appears twice starting at positions 12 and 24), 1322 (which appears twice at starting positions 2 and 29, and corresponds to the MLRY (SEQ ID NO:99) sequence described above) and 22 (appearing three times that do not overlap the longer coded subsequences at positions 7, 20 and

22). Our R_{temp} might then include one or any combination of these substrings representing hydrophobic free energy groups. Examples of appropriate sample subsequence templates might then include 33242221322, 13222233242, and 2233242221322 among others.

Please replace on page 79, line 7 to page 80, line 6 with the following amended paragraph:

Figures 4A-4D summarize the EAR responses to dopamine infusion with respect to the influence of SHQR (SEQ ID NO:1) and THQA (SEQ ID NO:2) in the two D_2DA receptor-transfected cell systems, in which the former significantly potentiated the dopamine-induced increment in total milli-pH units in both cell systems. We report the results of one-tailed t-tests with pairing within chamber as $t_{(\#)}$, where the # represents the degrees of freedom of the paired comparison and ρ denotes the probability of such results occurring by chance. For the SHQR (SEQ ID NO:1) peptide in the LtK system, $t_{(3)} = 13.28$, $\rho = 0.0009$, and for the SHQR (SEQ ID NO:1) peptide in the CHO cell system, $t_{(3)} = 28.06$, $\rho < 0.0001$. THQA (SEQ ID NO:2) did not significantly potentiate the dopamine response in either system, $t_{(3)} = 0.620$ and $t_{(3)} = 1.309$, $\rho > 0.05$, respectively. Figures 5A-5D contain graphs of the influence of the peptides E...PL (SEQ ID NO:3) and E...PY (SEQ ID NO:4) on the EAR response to dopamine in the two D_2DA receptor-transfected cell systems. Both peptides demonstrated statistically significant activation, $t_{(7)} = 25.47$, $\rho < 0.0001$ and $t_{(3)} = 69.830$, $\rho < 0.0001$, respectively, in the LtK system. However, neither of the E...PL (SEQ ID NO:3) and E...PY (SEQ ID NO:4) peptides influenced the dopamine-induced EAR of the CHO cells significantly, with $t_{(3)} = 1.542$, $\rho > 0.05$ and $t_{(7)} = 1.283$, $\rho > 0.05$, respectively. Three of the remaining eight peptides exhibited statistically significant effects on at least one of the two receptor-transfected cell systems (Table 3). The overall "hit rate", as measured by modulation of the kinetics of the EAR of two transfected cell lines to dopamine, for these peptides was thus 50% (i.e., six of twelve peptide candidates that were synthesized and tested statistically significantly altered EAR in one or both of the D_2DA receptor-transfected cell systems used). All D_2DA targeted peptides whose effects reached significance increased EAR.